RhUS28.1

```
        10         20         30         40         50         60
ATGAATAACA CATCTTGCAA CTTCAACGTC ACTCTCAACG CATCGGCACC AAGCCGATAC

        70         80         90        100        110        120
ATAGCTATTG CTATGTACAG CATTGTTATC TGTATCGGGT TGGTTGGAAA CCTGCTGTTA

       130        140        150        160        170        180
TGCATCGTGT TAGTCAAGAA ACGCAAACTG CGATATTCCA GCGATGTTTA TTTTTTCCAC

       190        200        210        220        230        240
GCCTCTATGG CCGACCTCGT CAGCACTGTC ATGCTACCGC TCTGGCTACA TTATGTCCTC

       250        260        270        280        290        300
AACTTTGCCC AACTCTCTCG AGGAGCCTGT ATCAGCTTTT CGGTGACTTT CTATGTTCCC

       310        320        330        340        350        360
CTTTTCGTTC AGGCCTGGTT ACTCATTTCC ATCGCTATGG AGCGATATTC CAACTTAGTA

       370        380        390        400        410        420
TGGATGGCAC CCATTAGCGT TAAGACGGCC TTTAAACACT GCATAGGAAC CTGGATCGTA

       430        440        450        460        470        480
TCTGCCTTCG TGGCATCACC CTACTACGCA TACAGAAACT CACACGACGA ACACGAATGC

       490        500        510        520        530        540
ATTCTAGGAA ACTACACTTG GCACATTAAC GAACCGCTAC ACACGTGTAT GGATGTGGTG

       550        560        570        580        590        600
ATCATAGTAT GGACCTTTTT GGCCCCAGTA CTGGTAACCA TTATAGCAAG CGTCAAAATG

       610        620        630        640        650        660
AGACGAACGA CCTGGGGCAA TACTAGGTTA AACGAAAAGA ACAGCGACAT TCTTATAGTA

       670        680        690        700        710        720
CTAGTTGTCA TGACAGTGTT CTTTTGGGGA CCGTTTAATA TCGTGTTGGT TATTGACAAT

       730        740        750        760        770        780
ATTTTACAGA GATACTATGA TACCACGAAT TGCGATGTAG AAAAGATTAA ACATATCATG

       790        800        810        820        830        840
GCTATGATCT CAGAAGCCAT TGTTTATTTT CGCGGTATTA CAGCACCTAT TATTTATGTA

       850        860        870        880        890        900
GGGATTAGTG GCAGATTTCG CGAAGAGATT TACTCTCTGT TTAGACGCCA GCCGTATAAC

       910        920        930        940        950        960
GATTTGGACC CCGATGCCAA TCAATTCATG ATTGAACTCA CTAGCCAGGG AAGAAGTAGA

       970        980        990       1000       1010       1020
AATAGAAATG CTAGACAATC GGAAAGCAAT GTACCGCAAC CAGAAGAATG CTTCTGGTAA

      1030       1040       1050       1060       1070       1080
.......... .......... .......... .......... .......... ..........
```

FIG. 1

RhUS28.2

```
        10          20          30          40          50          60
ATGACCAACG CCGGACACTG TCACATAAAC GAAAGTCTCG CGTCGTATGG AATCGCTCCC

        70          80          90         100         110         120
GCAGCTACCA TTACCTTATA CAGCATTGCG GGAATCTGCG GTGTCACGGG AAATCTGTTA

       130         140         150         160         170         180
ATACTTTTGG TTTTGTTCAC GAGACGCATA CACTGGTTCG CAAATGACAT CTACTATCTC

       190         200         210         220         230         240
AACATGATCT TTACAGACTT TCTTGTTTTC ATTACATTAC CCGCCTGGGT TTACTACCTG

       250         260         270         280         290         300
CTGAATTACA CACAACTCTC ACACTATGCC TGCATTGCTC TATCATTTGT TTTTTACGTT

       310         320         330         340         350         360
TCCATTTTTA TTCAAGCTGA CTTTATGGTA GCAGTGGCTA TCGAGCGTTA TCGAAGCCTA

       370         380         390         400         410         420
GTGAAAAACA AACCCCTTAG CGTAAAAAAA GCCAGCGTCA GCTGCGCGTG CATCTGGATC

       430         440         450         460         470         480
ATTGTTATTA TAGTGTCTTC ACCATACTAC ATGTTTAGAT CGCAACACGA AACAAATTCT

       490         500         510         520         530         540
TGCATTCTAG GAAACTACAC CTGGCATATG AACAGTCCTT TTCGCACCAC AATGGACGCA

       550         560         570         580         590         600
TCCATTAACA TTTGGTCTTT TGTCGTTCCG GCCGTGACGA CCTTGTTAAT AGCCAGACGA

       610         620         630         640         650         660
ATTTATGTAT GTACTTCAGG CAACAAAAAA ATGAACGCCA GAGCCAGTGG TTTGTTAGAG

       670         680         690         700         710         720
GCCATGGTGA TTAGCATGTT ATTCTTCGGA GGACTTTTCA ACCTGAACAT CTTTCGAGAC

       730         740         750         760         770         780
ATAGTTTCGG ACACATCGGA AGACAATAAA GACTGCACAT ATCTTAAGCA GGAACACTTT

       790         800         810         820         830         840
ATTCGCATGG TCGGTGTGGC CCTCGTTTAC GGGCGCGCTA TATTCAACCC TTTTATGTAT

       850         860         870         880         890         900
ATGTGTGTGA GTACCAGATT GCGCCAAGAA ATAAAATGTT TGTTTATGCG AATACCTTAT

       910         920         930         940         950         960
GAAACACTAG ATGCAGAACA CGCTAAACTC ATGGTTAATT TAAAAAACAG AAATGCTAAT

       970         980         990        1000        1010        1020
GTACCCGATC CTAAACCTCG TGAATATGAA TCTGTGTTAT AG..... ..........
```

FIG. 2

RhUS28.3

```
        10          20          30          40          50          60
ATGACCAACA CTAACAATAC GACTTGTCAT CTCAACGGAA CTTTCGAAAC TTTTAAAATC

        70          80          90         100         110         120
ACCCGTCCAG TAGCCATCAG CGCCTACACT GTACTCGTGG TTATCGGACT TTTGGGAAAC

       130         140         150         160         170         180
ATTGTGCTGC TCAGCGTGCT CGTCGTGAAA CGCAAGCTCA AGTTTCCGAA TGACATTTAC

       190         200         210         220         230         240
TTTTTCAACG CGTCTTTGGC AGACGTTTTT GCCGTCTGCA TGTTGCCCGC CTGGGTTAAC

       250         260         270         280         290         300
TATGCACTGG ACTCCACACA ACTTAGCAAG TTCTCATGTA TCACTTTTAC GTTTGGTTTT

       310         320         330         340         350         360
TACGTCTCCC TGTTCATCCA GGCCTGGATG CTCATTCTGG TCACCCTGGA GCGATACGGA

       370         380         390         400         410         420
TCTCTAGTCT GGATCGCCCC GATCACCAGA AACAAAGCCA TAGCGAATTG TGTACTCTTT

       430         440         450         460         470         480
TGGCTTGTTT CCATCTTCTT GGCCGCACCT TACTACTCTT TTAGAAACGA AAGCAACGAA

       490         500         510         520         530         540
CACCAATGCA TCATGAGAAA CTATACCTGG AGCGTTGGTG AAACATGGCA CATAGCCCTG

       550         560         570         580         590         600
GATTTCTTAA TTACGCTCAT TACATTTATC ATGCCAGTGA CTATTGTGTT AGCTCTGAGT

       610         620         630         640         650         660
TTCAAAATGG CCAGATGGTC AACCTTTGGT TACAGAAACC TCACCAGCAG AACCAGTCTT

       670         680         690         700         710         720
ATCCTTATTT TGATACTGAC AGTAGCAGCA GGGTTCTGGG GACCTTTTCA CCTATTTATG

       730         740         750         760         770         780
TTTATAGAAA ACGTGGCAGG GCAGATTTAC CACATTCAAA AGGATTGCTG GTACTTACAG

       790         800         810         820         830         840
CTCAGACACT TGTGTAGCTT GATGACCGAA ACCCTAGTGT TTCTACGTTC AGTTTTTAAC

       850         860         870         880         890         900
CCTTATATTT ATATGATAAT CAGTTACAAG TTTAGGCAGC AGGTGCGCAG TCTACTCAAG

       910         920         930         940         950         960
CGTACTCAGT ATGATGCTTT GGACACGACT CAGTTAGCAG AAACTATGCA GCTGAAAGCG

       970         980         990        1000        1010        1020
AAAGGTGTGC CGGTGTCCGA CCCCGCGCCG CATGACTGCG AATGCTTTTT GTAA......
```

FIG. 3

RhUS28.4

```
        10         20         30         40         50         60
GAATTCGAGC CAGCACAACA TAAGCGTGTT TCTCTCCATT GGAGCAGGGC CCGTCATTAC

        70         80         90        100        110        120
CGGATACACG TGCGTTTTTC TGTTCGGGAT TCTGGGACAC TTTTACTTGT ATTGGAAAAA

       130        140        150        160        170        180
CCATCAGAGA CGACACCGGA CAAACAGTTT CAGTGATGTT TTATTTCGAC ATCTCATGAT

       190        200        210        220        230        240
CACCGAAGAG GTCTTTACCC TCACCATTCC CGTCTGGGCG TATCACTTAA CTACTCACGG

       250        260        270        280        290        300
CAACTTACCG GGCTCGTGGT GCCGAAGTCT CACCTTCGTT TTTTATCTAA CGGTATTCGC

       310        320        330        340        350        360
TCGTGCCTTC TTTTACCTGC TCCTCATCTG GGACCGATAC AGCGTAATCA TCTGCAGACA

       370        380        390        400        410        420
CCCTCTCCCC GTTAATCTGA ACTACAGTCA GGTCATAGGC CTGTCTGTCT GGCTGGTTGC

       430        440        450        460        470        480
CGTACTGTCA GCATCACCGT TCTCCATTTT TAACGGAAGT GTGAAACAAT GCCTGGGCAA

       490        500        510        520        530        540
CATGGGCAGC ATACCCAGCG AATCGTCTGC CGTTCTTAAC CTGGAAGTGC ACCTGTGCTC

       550        560        570        580        590        600
CTTCTGGTTA CCGCTCATCA TGTCGGCTAA CTGTTACTAC CAAGCAAAAC GCCGAGCATC

       610        620        630        640        650        660
GCCTGACCAA CTCCACGAAC TTTACCGATG CAGTTTGCTA ATTACCATTA TCACAACTTA

       670        680        690        700        710        720
CGCTATCGTA TGGTTTCCTT TCCATCTCGC TTTACTCATA GACGCCCTGA TTAGCATAAG

       730        740        750        760        770        780
CCATGTAGAA CCCTCTAGCG CTCTCCACTG GGCATCCATT GTCGTTACCT GTAAATCATT

       790        800        810        820        830        840
TACATTTGTA TATGCGGGCA TAAGCCCACT AGTGTATTTC ACATGCTGCC CCACCGTACG

       850        860        870        880        890        900
TCGCGAACTG CTGATGTCTC TACGTCCATT CTTCACCTGG ATTTCCAGCA AAACGCGGCG

       910        920        930        940        950        960
AGGCTACGCT CCGATTAAAA CACAACCTTT AAACATCCCC GACGAGCCGA TAGATAACAA

       970        980        990       1000       1010       1020
GTCACCGCAC CTGTTAAACG AATAA..... .......... .......... ..........
```

FIG. 4

Rhus28.5

```
        10         20         30         40         50         60
ATGACTACCA CCACAATGAG TGCTACCACG AATTCCAGTA CCACGCCTCA AGCAAGCAGC

        70         80         90        100        110        120
ACCACGATGA CAACGAAGAC AAGCACTCCT GGCAATACAA CTACTGGCAC TACGTCCACC

       130        140        150        160        170        180
CTGACAACGA TATCAACAAC TTCTAATGCT ACCAGCATAA CGTCTAATTT AAGCACTACC

       190        200        210        220        230        240
GGAAACCAAA CTGCAACTAC CAATGCTACT ACCTTCAGTT CCACATTAAC AACATCTACA

       250        260        270        280        290        300
AATATAAGCA GTACATTTTC GACAGTTTCT ACCGTCGCAT CCAATGCAAC ATGTAATTCT

       310        320        330        340        350        360
ACAATCACAA CGAATATTAC AACTGCTTTT ACTACAGCAG CAAACACTAC CGCAAGCAGC

       370        380        390        400        410        420
CTCACCAGCA TCGTAACTTC ACTTGCCACT ACCATTGAAA CCACATCATT TGATTATGAT

       430        440        450        460        470        480
GAGTCAGCAG AAGCTTGCAA CTTAACAGAC ATCGTTCATA CTACTAGATC AGTGACAGTT

       490        500        510        520        530        540
ACTTTCTATA CTATCATATT CATACTCGGC CTTTTGGGAA ACTTTCTGGT TCTTATGACC

       550        560        570        580        590        600
ATCATTTGGA ACCGTCGCAT TTCCTTTATG GTTGAAATAT ATTTCGTTAA TCTAGCAATC

       610        620        630        640        650        660
TCCGATCTTA TGTTTGTATG TACTTTACCA TTTTGGATAA TGTATCTTCT TGAGCACGAC

       670        680        690        700        710        720
GTCATGTCAC ATGCATCCTG TGTAGCAATG ACAGCCATTT TTTATTGCGC GCTGTTTGCC

       730        740        750        760        770        780
AGCACTGTTT TCCTCTTGCT AATTGTTTTA GACAGATGTT ACGCTATTCT ATTAGGTACA

       790        800        810        820        830        840
GAAAAAGCAA ATAGACGTTT ATTGCGCAAT GCTGTTTCTG GATGCATGCT CATGTGGGGA

       850        860        870        880        890        900
TTGTGTTTCA TTTTAGCATT ACCTCATTTT ATCTTTATGA AGAAAGGAAC CAACGTATGT

       910        920        930        940        950        960
GTAGCAGAGT ATGAACCAGG ACTTAACAAT TTCTATGTTA TTTTTATCAA TACTGAGGTG

       970        980        990       1000       1010       1020
AACCTATGCA CCCTAGTTTT GCCAGCCGCA GCCATTATCT ACTGGTATCT TAAACTAACC

      1030       1040       1050       1060       1070       1080
AAAGCACTCA AAACCCATGA ACGACTGCGT CATAGGCTAA CGTCTCTAAA CATAGTGTTA

      1090       1100       1110       1120       1130       1140
GCTGTTGTCA TTGTATTTGC TTTGTTTTGG CTGCCGTATA ATCTCATGCT TATGATGTAT

      1150       1160       1170       1180       1190       1200
AGCTTAGTTC ACATGCAGAT ACCTTGGGAA TGCAGCTCTG AAAAAATACT GAGACGAAGT

      1210       1220       1230       1240       1250       1260
TTAATTATTA CAGAATCCAT CGCCCTCAGT CACTGTTGCA TCAACCCCAT TATCTACTTG
```

FIG. 5A

RhUS28.5

```
      1270       1280       1290       1300       1310       1320
CTCTTCGGAC CTCGCTGTCG AAGCGAGTTC TGTCACCTGT TGCGATGTTG CTTTACGCGC

      1330       1340       1350       1360       1370       1380
TTATGTCCAC ACAGATCCTG GAGTTCCATA CGTGCAGAGA CGGTGTCCAT CAGTCTCAGT

      1390       1400       1410       1420       1430       1440
CACTCACAGG TATCTGCATC ATCTGAGGAT GATGACAACG ATGTGCATGA TGAATTGCAA

      1450       1460       1470       1480       1490       1500
TTTTTAATTT GA..... ..... ..... ..... ..... .....
```

FIG. 5B

RhUL33

```
        10          20          30          40          50          60
ATGACCAATC TTTACTCTGC CAATTTTCTC ACCTTGATAG TACTTCCTTT TATCGTTTTA

        70          80          90         100         110         120
AGCAATCAAC ACCTTTTACC TGCCAGTGCA GTAACCTGTA AATTTCTCTC CCTGTTGTAC

       130         140         150         160         170         180
TACTCTAGCT GCAGCGTAGG TTTTGCTACA GTGGCACTGA TAGCGGCCGA CCGATACCGA

       190         200         210         220         230         240
GTGATTCATC GCCGAACTCA AGCTCGCCAA TCCTACCGTA ACACATATAT GATAGTAGGC

       250         260         270         280         290         300
TTAACGTGGC TCATTGGCTT GATCTGCGCT ACCCCCGGGG GGGTCTACAC AACCATTGTA

       310         320         330         340         350         360
GCTCACCGCG ATGGGGAAAG TGATGCTCAA AGACACAATA CTTGCATTAT GCACTTTGCG

       370         380         390         400         410         420
TATGATGAAG TTTACGTCCT CATGGTCTGG AAACTTCTCA TCGTTTTAGT CTGGGGCATA

       430         440         450         460         470         480
GTGCCAGTTG TCATGATGAG CTGGTTTTAC GCGTTTTTTT ACAATACTGT ACAAAGAACA

       490         500         510         520         530         540
GCCAAAAAAC AACAACGTAC GTTGAAATTC GTAAAGGTAT TACTCCTGTC ATTCATCATC

       550         560         570         580         590         600
ATCCAAACTC CCTATGTGTC AATCATGATT TTTAACACGT ATGCCACCGT AGGATGGCCG

       610         620         630         640         650         660
ATGGAATGCG CCGATCTAAC TAGACGCCGA GTCATCAACA CGTTTTCCCG TCTCGTCCCC

       670         680         690         700         710         720
AATCTACATT GCATGGTCAA CCCCATCCTC TACGCTCTCA TGGGAAATGA CTTTGTGTCT

       730         740         750         760         770         780
AAAGTGGGCC AATGCTTTCG GGGGGAACTC ACGAACCGTC GAACTTTTCT GCGTTCCAAG

       790         800         810         820         830         840
CAACAAGCCC GCAACTCGGA CGATGTACCG ACAATTGTCA GTCAACAACC CGCCACACCC

       850         860         870         880         890         900
ACCATCGTCA ATAAGCCCGA AAAAAACCCG CACGTAAAAC GCGGTGTATC TTTCAGCGTC

       910         920         930         940         950         960
AGCGCATCTT CCGAACTCGC AGCGGCCAAA AAAGCCAAAG ACAAAGCCAA GCGGCTTTCC

       970         980         990        1000        1010        1020
ATGTCCCACC AAAACCTACG TCTGACGTGA .......... .......... ..........
```

FIG. 6

RhUL33 spliced

```
        10         20         30         40         50         60
ATGGCAGTCA CTTTACGAGG CGGCAGCCCG ATAAACTTTA AACTCATGAT TGTCAGCCAC

        70         80         90        100        110        120
AGAAACCGGA AATTTCACGA GATACGGCTG TTTCAGCGTT CTGCTATCCG TCCAGGCGGG

       130        140        150        160        170        180
TTATGGAAAC CATTCTTCAC AACCGAACG- ---------- ---------- ----------

       190        200        210        220        230        240
---------- ---------- ---------- ---------- -----AGTGA AACTAATTCC

       250        260        270        280        290        300
ATTTTGCACA TCAACACCAC CTGCAATGTG ACCGACTCAC TGTACGCCGC CAAACTAGGC

       310        320        330        340        350        360
GAAGCCCTCG TGAACAGCGC GCTAGCTTTA TTCGGTACCC CCCTCAACGC CATCGTCCTC

       370        380        390        400        410        420
GTCACACAGC TATTGGCCAA CCGAGTTCAT GGATACTCCA CCCCGATTAT CTACATGACC

       430        440        450        460        470        480
AATCTTTACT CTGCCAATTT TCTCACCTTG ATAGTACTTC CTTTTATCGT TTTAAGCAAT

       490        500        510        520        530        540
CAACACCTTT TACCTGCCAG TGCAGTAACC TGTAAATTTC TCTCCCTGTT GTACTACTCT

       550        560        570        580        590        600
AGCTGCAGCG TAGGTTTTGC TACAGTGGCA CTGATAGCGG CCGACCGATA CCGAGTGATT

       610        620        630        640        650        660
CATCGCCGAA CTCAAGCTCG CCAATCCTAC CGTAACACAT ATATGATAGT AGGCTTAACG

       670        680        690        700        710        720
TGGCTCATTG GCTTGATCTG CGCTACCCCC GGGGGGGTCT ACACAACCAT TGTAGCTCAC

       730        740        750        760        770        780
CGCGATGGGG AAAGTGATGC TCAAAGACAC AATACTTGCA TTATGCACTT TGCGTATGAT

       790        800        810        820        830        840
GAAGTTTACG TCCTCATGGT CTGGAAACTT CTCATCGTTT TAGTCTGGGG CATAGTGCCA

       850        860        870        880        890        900
GTTGTCATGA TGAGCTGGTT TTACGCGTTT TTTTACAATA CTGTACAAAG AACAGCCAAA

       910        920        930        940        950        960
AAACAACAAC GTACGTTGAA ATTCGTAAAG GTATTACTCC TGTCATTCAT CATCATCCAA

       970        980        990       1000       1010       1020
ACTCCCTATG TGTCAATCAT GATTTTTAAC ACGTATGCCA CCGTAGGATG GCCGATGGAA

      1030       1040       1050       1060       1070       1080
TGCGCCGATC TAACTAGACG CCGAGTCATC AACACGTTTT CCCGTCTCGT CCCCAATCTA

      1090       1100       1110       1120       1130       1140
CATTGCATGG TCAACCCCAT CCTCTACGCT CTCATGGGAA ATGACTTTGT GTCTAAAGTG

      1150       1160       1170       1180       1190       1200
GGCCAATGCT TTCGGGGGGA ACTCACGAAC CGTCGAACTT TTCTGCGTTC CAAGCAACAA

      1210       1220       1230       1240       1250       1260
GCCCGCAACT CGGACGATGT ACCGACAATT GTCAGTCAAC AACCCGCCAC ACCCACCATC
```

FIG. 7A

RhUL33 spliced

```
      1270       1280       1290       1300       1310       1320
GTCAATAAGC CCGAAAAAAA CCCGCACGTA AAACGCGGTG TATCTTTCAG CGTCAGCGCA

      1330       1340       1350       1360       1370       1380
TCTTCCGAAC TCGCAGCGGC CAAAAAAGCC AAAGACAAAG CCAAGCGGCT TTCCATGTCC

      1390       1400       1410       1420       1430       1440
CACCAAAACC TACGTCTGAC GTGA...... .......... .......... ..........
```

FIG. 7B

RhUL78

```
        10         20         30         40         50         60
ATGATTACGG AGCGCGTCCT CGCAGGCATC CTCGCGGGCA TGACGGCCGC GGGGAGTTTG

        70         80         90        100        110        120
GTCATTCTCC TCGCGGTTGT TATGTGGTTG AACATGTTAG ATCGCGCTGG CATGCCAATG

       130        140        150        160        170        180
GCCGTTGGGC ATTACACAGG GAACCTGGTG TTGACTCAGG TCATCTGTAT CTTCTCCATG

       190        200        210        220        230        240
CTGGCGTCTA AAATTGTTGG CATGACGAGT GCGGCCAACA TGGGCTTCTG CGGCATCGTG

       250        260        270        280        290        300
GTTTTTCTGG AAGACACTGG CCTCTATGTC ACCTCGCTGC TCTTCATGTT TATGATCCTG

       310        320        330        340        350        360
GATCGCATGG CGGCTTTTCT TAACGGGCGT CTTTTCTGGA GGCAGCAGAC GACGAAGCAG

       370        380        390        400        410        420
AATCTGAGTA CAAGCGTGTA CATTATTCTG TTTTGCTGGG TGTTGGGAAT GGCCGCGGCT

       430        440        450        460        470        480
GTTCCCAGCG CGGCTGTGGC TGCACCCAAT TCCAGGTGGG AACGCTGCGA AATTCCAGTG

       490        500        510        520        530        540
TCATATGCCG CAATCGACAT GATTGTGAAG CTCTGGTTTG TGCTGTTGGC ACCCGTCGTG

       550        560        570        580        590        600
CTGATTATGG CTGTGATCAT TCAATCTTCC TATCATCGTG ATCGGGAGAG GATCTGGTAC

       610        620        630        640        650        660
TATGCCAGAC GTGTGTTCAT GTTCTACACG GCCTGCTTTG TCATGATGGT GCCTTATTAC

       670        680        690        700        710        720
TTCGTCAGAG TCATGCTGAG CGACTTTGCT TTGGTTGATA TAAAAACAAA AACGGCGAAC

       730        740        750        760        770        780
AGCGACGGTT GTGATTCGAC ATTTCTTGAT TATCTGAACA TGTTCACTCA CGTGATTTAC

       790        800        810        820        830        840
AGTTTTAAGT TGGTGGTGTT TGCTTTGTTC ATTGTCCTGT TTTGCTCCAT AAACCCGATG

       850        860        870        880        890        900
GAAACGCTGG AAGAATGCTT GGAGAGGGCC GATGCTGAGA GGCAAAGTCG GTCAGAAGCA

       910        920        930        940        950        960
TCCCAGGGTG AAAGGAGGCT GCCAATCAAC ACATGCTGTA TAAAGTTGAT TGAATTGATA

       970        980        990       1000       1010       1020
AAGCAGTATG TAAGCACTCT CTCTAAAGCC ACGAGGGACA ATTCTGGCGA AAGGGCCAAT

      1030       1040       1050       1060       1070       1080
TTGCCAGAGA ATGCTGAAGA TATTGGAACA ACTGGCAGTG ATCAGCTACC GACTGAGGTC

      1090       1100       1110       1120       1130       1140
ACCGTGACCC CAAATTCATC GGCTGTGTTT AGCACTGGAG GAACGGTGTC TCCAGTCTAA

      1150       1160       1170       1180       1190       1200
.......... .......... .......... .......... .......... ..........
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FIG. 8